RAW SEQUENCE LISTING   DATE: 11/06/2001
PATENT APPLICATION: US/09/856,812   TIME: 14:59:21

Input Set : **A:\PTO.DC.txt**
Output Set: **N:\CRF3\11062001\I856812.raw**

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 3 <110> APPLICANT: Huang, Lan-Qing
 4         Van Pel, Aline
 5         Brasseur, Francis
 6         De Plaen, Etienne
 7         Boon, Thierry
 9 <120> TITLE OF INVENTION: Tumour Rejection Antigens
11 <130> FILE REFERENCE: L0461/7115(JRV)
13 <140> CURRENT APPLICATION NUMBER: US 09/856,812
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C--> **14 <141> CURRENT FILING DATE: 2001-09-07**
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16 <150> PRIOR APPLICATION NUMBER: GB 9826143.1
17 <151> PRIOR FILING DATE: 1998-11-27
19 <160> NUMBER OF SEQ ID NOS: 56
21 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapiens
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35 Ala Val Glu Glu Asp Ala Ser Ser Ser Thr Ser Thr Ser Ser Ser Phe
36          35                  40                  45
38 Pro Ser Ser Phe Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Tyr
39       50                  55                  60
41 Pro Leu Ile Pro Ser Thr Pro Glu Glu Val Ser Ala Asp Asp Glu Thr
42  65                  70                  75                  80
44 Pro Asn Pro Pro Gln Ser Ala Gln Ile Ala Cys Ser Ser Pro Ser Val
45                  85                  90                  95
47 Val Ala Ser Leu Pro Leu Asp Gln Ser Asp Glu Gly Ser Ser Ser Gln
48              100                 105                 110
50 Lys Glu Glu Ser Pro Ser Thr Leu Gln Val Leu Pro Asp Ser Glu Ser
51          115                 120                 125
53 Leu Pro Arg Ser Glu Ile Asp Glu Lys Val Thr Asp Leu Val Gln Phe
54       130                 135                 140
56 Leu Leu Phe Lys Tyr Gln Met Lys Glu Pro Ile Thr Lys Ala Glu Ile
57 145                 150                 155                 160
59 Leu Glu Ser Val Ile Lys Asn Tyr Glu Asp His Phe Pro Leu Leu Phe
60              165                 170                 175
62 Ser Glu Ala Ser Glu Cys Met Leu Leu Val Phe Gly Ile Asp Val Lys
63          180                 185                 190
65 Glu Val Asp Pro Thr Gly His Ser Phe Val Leu Val Thr Ser Leu Gly
66          195                 200                 205
68 Leu Thr Tyr Asp Gly Met Leu Ser Asp Val Gln Ser Met Pro Lys Thr
69       210                 215                 220
71 Gly Ile Leu Ile Leu Ile Leu Ser Ile Ile Phe Ile Glu Gly Tyr Cys
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78             260                265                270
80 Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly
81         275                280                285
83 Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala
84     290                295                300
86 Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly
87 305                310                315                320
89 Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp
90             325                330                335
92 Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr
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114 Ala Glu Glu Gln Lys Ala Ala Ser Ser Ser Ser Thr Leu Ile Met Gly
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117 Thr Leu Glu Glu Val Thr Asp Ser Gly Ser Pro Ser Pro Pro Gln Ser
118     50                55          .        60
120 Pro Glu Gly Ala Ser Ser Ser Leu Thr Val Thr Asp Ser Thr Leu Trp
121 65                70                75                80
123 Ser Gln Ser Asp Glu Gly Ser Ser Ser Asn Glu Glu Glu Gly Pro Ser
124             85                90                95
126 Thr Ser Pro Asp Pro Ala His Leu Glu Ser Leu Phe Arg Glu Ala Leu
127         100                105                110
129 Asp Glu Lys Val Ala Glu Leu Val Arg Phe Leu Leu Arg Lys Tyr Gln
130         115                120                125
132 Ile Lys Glu Pro Val Thr Lys Ala Glu Met Leu Glu Ser Val Ile Lys
133     130                135                140
135 Asn Tyr Lys Asn His Phe Pro Asp Ile Phe Ser Lys Ala Ser Glu Cys
136 145                150                155                160
138 Met Gln Val Ile Phe Gly Ile Asp Val Lys Glu Val Asp Pro Ala Gly
139             165                170                175
141 His Ser Tyr Ile Leu Val Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu
142             180                185                190
144 Leu Gly Asp Asp Gln Ser Thr Pro Lys Thr Gly Leu Leu Ile Ile Val
145         195                200                205
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167 gctttgggaa tcccatgcag gtgtgatcgt gtggtgcccc tccccacttc tgcctgccgg 240
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171 gttcttagct ctgaggggac ctgatcagga ttggcactaa gtggcaagct caattttacc 480
172 acaggcagga agatgaggaa ccctcaggga aatggagttt tggtgtaaag gggagatatc 540
173 agccctggac accccacagg gatgacagga tgtggctcct tcttactttt gttttggaat 600
174 ctcagggagg tgagaacctt gctctcagag ggtgactcaa gtcaacacag ggaacccctc 660
175 ttttctacag acacagtggg tcgcaggatc tgacaagagt ccaggtaagg aacctgaggg 720
176 aaatctgagg gtaccccag cccataacac agatggggtc cccacagaaa tctgccatga 780
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195 ggccacttac accctccctc tctccccagg cctgtgggtc cccatcgccc aagtcctgcc 1920
197 cacactccca cctgctaccc tgatcagagt catc atg cct cga gct cca aag cgt 1975
198                                       Met Pro Arg Ala Pro Lys Arg
199                                       1               5
201 cag cgc tgc atg cct gaa gaa gat ctt caa tcc caa agt gag aca cag  2023
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209 tca tcc act tcc acc agc tcc tct ttt cca tcc tct ttt ccc tcc tcc      2119
210 Ser Ser Thr Ser Thr Ser Ser Ser Phe Pro Ser Ser Phe Pro Ser Ser
211 40                    45                    50                    55
213 tcc tct tcc tcc tcc tcc tcc tgc tat cct cta ata cca agc acc cca      2167
214 Ser Ser Ser Ser Ser Ser Ser Cys Tyr Pro Leu Ile Pro Ser Thr Pro
215                   60                    65                    70
217 gag gag gtt tct gct gat gat gag aca cca aat cct ccc cag agt gct      2215
218 Glu Glu Val Ser Ala Asp Asp Glu Thr Pro Asn Pro Pro Gln Ser Ala
219                   75                    80                    85
221 cag ata gcc tgc tcc tcc ccc tcg gtc gtt gct tcc ctt cca tta gat      2263
222 Gln Ile Ala Cys Ser Ser Pro Ser Val Val Ala Ser Leu Pro Leu Asp
223       90                    95                    100
225 caa tct gat gag ggc tcc agc agc caa aag gag gag agt cca agc acc      2311
226 Gln Ser Asp Glu Gly Ser Ser Ser Gln Lys Glu Glu Ser Pro Ser Thr
227       105                   110                   115
229 cta cag gtc ctg cca gac agt gag tct tta ccc aga agt gag ata gat      2359
230 Leu Gln Val Leu Pro Asp Ser Glu Ser Leu Pro Arg Ser Glu Ile Asp
231 120                   125                   130                   135
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234 Glu Lys Val Thr Asp Leu Val Gln Phe Leu Leu Phe Lys Tyr Gln Met
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237 aag gag ccg atc aca aag gca gaa ata ctg gag agt gtc ata aaa aat      2455
238 Lys Glu Pro Ile Thr Lys Ala Glu Ile Leu Glu Ser Val Ile Lys Asn
239                   155                   160                   165
241 tat gaa gac cac ttc cct ttg ttg ttt agt gaa gcc tcc gag tgc atg      2503
242 Tyr Glu Asp His Phe Pro Leu Leu Phe Ser Glu Ala Ser Glu Cys Met
243       170                   175                   180
245 ctg ctg gtc ttt ggc att gat gta aag gaa gtg gat ccc act ggc cac      2551
246 Leu Leu Val Phe Gly Ile Asp Val Lys Glu Val Asp Pro Thr Gly His
247       185                   190                   195
249 tcc ttt gtc ctt gtc acc tcc ctg ggc ctc acc tat gat ggg atg ctg      2599
250 Ser Phe Val Leu Val Thr Ser Leu Gly Leu Thr Tyr Asp Gly Met Leu
251 200                   205                   210                   215
253 agt gat gtc cag agc atg ccc aag act ggc att ctc ata ctt atc cta      2647
254 Ser Asp Val Gln Ser Met Pro Lys Thr Gly Ile Leu Ile Leu Ile Leu
255                   220                   225                   230
257 agc ata atc ttc ata gag ggc tac tgc acc cct gag gag gtc atc tgg      2695
258 Ser Ile Ile Phe Ile Glu Gly Tyr Cys Thr Pro Glu Glu Val Ile Trp
259                   235                   240                   245
261 gaa gca ctg aat atg atg ggg ctg tat gat ggg atg gag cac ctc att      2743
262 Glu Ala Leu Asn Met Met Gly Leu Tyr Asp Gly Met Glu His Leu Ile
263       250                   255                   260
265 tat ggg gag ccc agg aag ctg ctc acc caa gat tgg gtg cag gaa aac      2791
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271 280                   285                   290                   295
273 ttt ctg tgg ggt cca agg gct cat gct gaa att agg aag atg agt ctc   2887
274 Phe Leu Trp Gly Pro Arg Ala His Ala Glu Ile Arg Lys Met Ser Leu
275                   300                   305                   310
277 ctg aaa ttt ttg gcc aag gta aat ggg agt gat cca aga tcc ttc cca   2935
278 Leu Lys Phe Leu Ala Lys Val Asn Gly Ser Asp Pro Arg Ser Phe Pro
279                   315                   320                   325
281 ctg tgg tat gag gag gct ttg aaa gat gag gaa gag aga gcc cag gac   2983
282 Leu Trp Tyr Glu Glu Ala Leu Lys Asp Glu Glu Glu Arg Ala Gln Asp
283         330                   335                   340
285 aga att gcc acc aca gat gat act act gcc atg gcc agt gca agt tct   3031
286 Arg Ile Ala Thr Thr Asp Asp Thr Thr Ala Met Ala Ser Ala Ser Ser
287     345                   350                   355
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297 atgataaatg catgaggtga tggatacact acctgatttg atcattatac tacatataca 3384
298 tgaatcagaa catcaaattg tacctcataa atatctacaa ttacatgtca gtttttgttt 3444
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325 tccttgtcac ctccctgggc ctcacctatg atgggatgct gagtgatgtc cagagcatgc 1020
326 ccaagactgg cattctcata cttatcctaa gcataatctt catagagggc tactgcaccc 1080
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L:463 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5